AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 10, line 28, with the following amended paragraph:

From the group of R2 rice plants (self-crossed progeny from the NC0608 strain) obtained according to Example 2, individuals exhibiting mutation were identified from normal individuals. DNA was prepared from both groups of individuals by using a CTAB method (Murray and Thompson, 1980, Nucleic Acids Res. 8, 4321-4325). The DNA obtained from individuals exhibiting narrow-leaf mutation and the DNA obtained from normal individuals were each digested with restriction enzyme XbaI, and after agarose electrophoresis, were allowed to adsorb to nylon membranes. DNA fragments which were obtained from Tos17 through digestion by XbaI and BamHI were labeled with ^{32}P-dCTP. By using these as probes, a Southern hybridization was performed (FIG. 2, left). As seen from the Southern analysts autoradiogram shown on the left-hand side in FIG. 2, it was learned the Tos17 band (about 6600 bp) indicated by an arrow was observed in narrow-leaf mutations as a homozygous band, but not in normal individuals, and that the Tos17 band indicated by the arrow was completely linked with the narrow-leaf mutation phenotype. From these results, it was concluded that the DNA which is represented by the band which hybridizes to the Tos17 probe indicated by the arrow contains a causative gene, such that Tos17, when inserted in a genome region represented by this band, generates narrow-leaf mutations as the genotype becomes homozygous. Accordingly, a portion of the causative gene for the narrow-leaf mutations, i.e., a sequence adjoining Tos17, was isolated through TAIL-PCR reactions using this DNA as a template. The amplification of the Tos17 target site sequence was accomplished by TAIL-PCR employing the total DNA (Liu Y -G. et al., 1995, Genomios, 25, 674-681, Liu Y -G. et al., 1995, Plant J., 8, 457-463). In summary, by using as a template the total DNA from a regenerated plant having a new Tos17 target site, three TAIL-PCR amplification reactions were performed, using the following three sets of primers: (1st reaction) Tos17 Tail3, GAGAGCATCATCGGTTACATCTTCTC (SEQ ID NO: 4) and AD1 (arbitrarily degenerated primer 1) NGTCGA (G/C) (A/T) GANA (A/T)

GAA; (2nd reaction) Tos17 Tail4, ATCCACCTTGAGTTTGAAGGG (SEQ ID NO: 5) and AD1; and (3rd reaction) Tos17 Tail5, CATCGGATGTCCAGTCCATTG (SEQ ID NO: 6) and AD1. Next, the respective TAIL-PCR products were subjected to an agarose electrophoresis and then a simple column purification. By directly applying them to a sequencer (Model 377 available from ABI), sequencing was performed.

Please replace the paragraph beginning on page 13, line 27, with the following amended paragraph:

First step: Using cDNA library as a template, a PCR reaction was carried out by using a pair of primers specific to the adjoining sequence NC0608_0_102 to confirm that a portion of this adjoining sequence is contained in the cDNA library: NC0608_0_102F ACGGAGACACCTCGTAAACC (SEQ ID NO: 7) and NC0608_0_102R1 AAGGCCGACTATTGTTGACC (SEQ ID NO: 8).

Please replace the paragraph beginning on page 14, line 8, with the following amended paragraph:

Third step: Using the cDNA library as a template, a PCR reaction was carried out by using Hybri ZAP A (Stratagene), which is a primer specific to Hybri ZAP-II vector, and NC0608_0_102R2 CCTGCAATGTTACCTCTGGC (SEQ ID NO: 9), which is a primer specific to NC0608_0_102. Thus, a 5' fragment which partially overlaps with NC0608_0_102 was obtained.

Please replace the paragraph beginning on page 14, line 15, with the following amended paragraph:

Fourth step: Using Cap Site cDNA (Nipponegne) as a template, a PCR reaction was carried out by using 1RC2 (Nippongene), which is a primer specific to Cap Site, and TGACAGGTCAGACTGATCAACCGG (SEQ ID NO: 10), which is a primer specific to the fragment obtained in the third step. Thus, a fragment which partially overlaps with the fragment obtained in the third step and which contains the 5' region of cDNA along with the transcription start point (cap site).

Please replace the paragraph beginning on page 14, line 26, with the following amended paragraph:

First step: Using the total DNA of Nipponbare, two reactions of TAIL-PCR were carried out using the following two sets of primers to obtain a 5' fragment which partially overlaps with the NC0608_0_102: (first reaction: NC0608_0_102R2 and AD1 employed in Example 3; second reaction: NC0608_0_102R3 TAGGCAATCCGGCAATGTCC (SEQ ID NO: 11) and AD1)

Please replace the paragraph beginning on page 14, line 33, with the following amended paragraph:

Second step: Using the total DNA of Nipponbare, a PCR reaction was carried out using a primer (CTAGAAGCAAAATCTTGAAGCTGC) (SEQ ID NO: 12) which is specific to the fragment obtained in the first step and a primer (AGTGTTCTTCGCACCTCGCG) (SEQ ID NO: 13) which is specific to the cDNA

fragment obtained in the fourth step PCR. Thus, a 5' fragment which partially overlaps with the fragment obtained in the first step was obtained.

Please replace the paragraph beginning on page 15, line 9, with the following amended paragraph:

Third step: Using the total DNA of Nipponbare, a PCR reaction was carried out using a primer (TGCCTCGCCCTCGGCGATGG) (SEQ ID NO: 14) which is specific to the fragment obtained in the second step and a primer (AATATTTCAAATCACACTAC) (SEQ ID NO: 15) which is specific to the 5' region of the cDNA fragment obtained in the fourth step PCR. Thus, a 5' fragment which partially overlaps with the fragment obtained in the second step was obtained.